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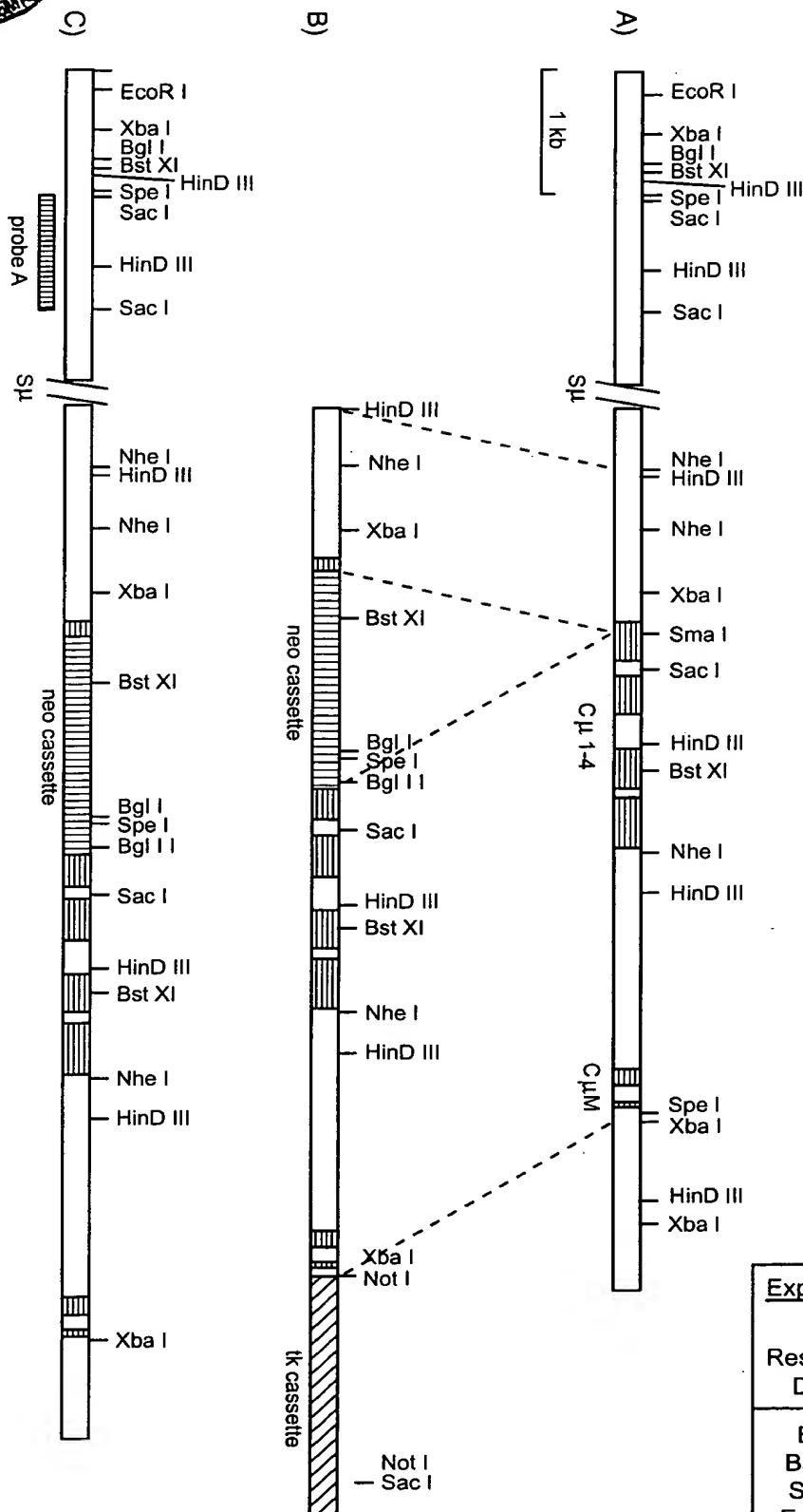
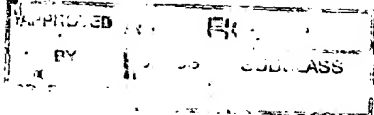


FIG. 1

Expected Fragment Sizes (kb) using Probe A		
Restriction Digest	Fragment Length	
	wild type	mutant
Bgl I	15.7	7.7
Bst XI	7.3	6.6
Spe I	9.9	7.6
Eco R I	12.5	14.3



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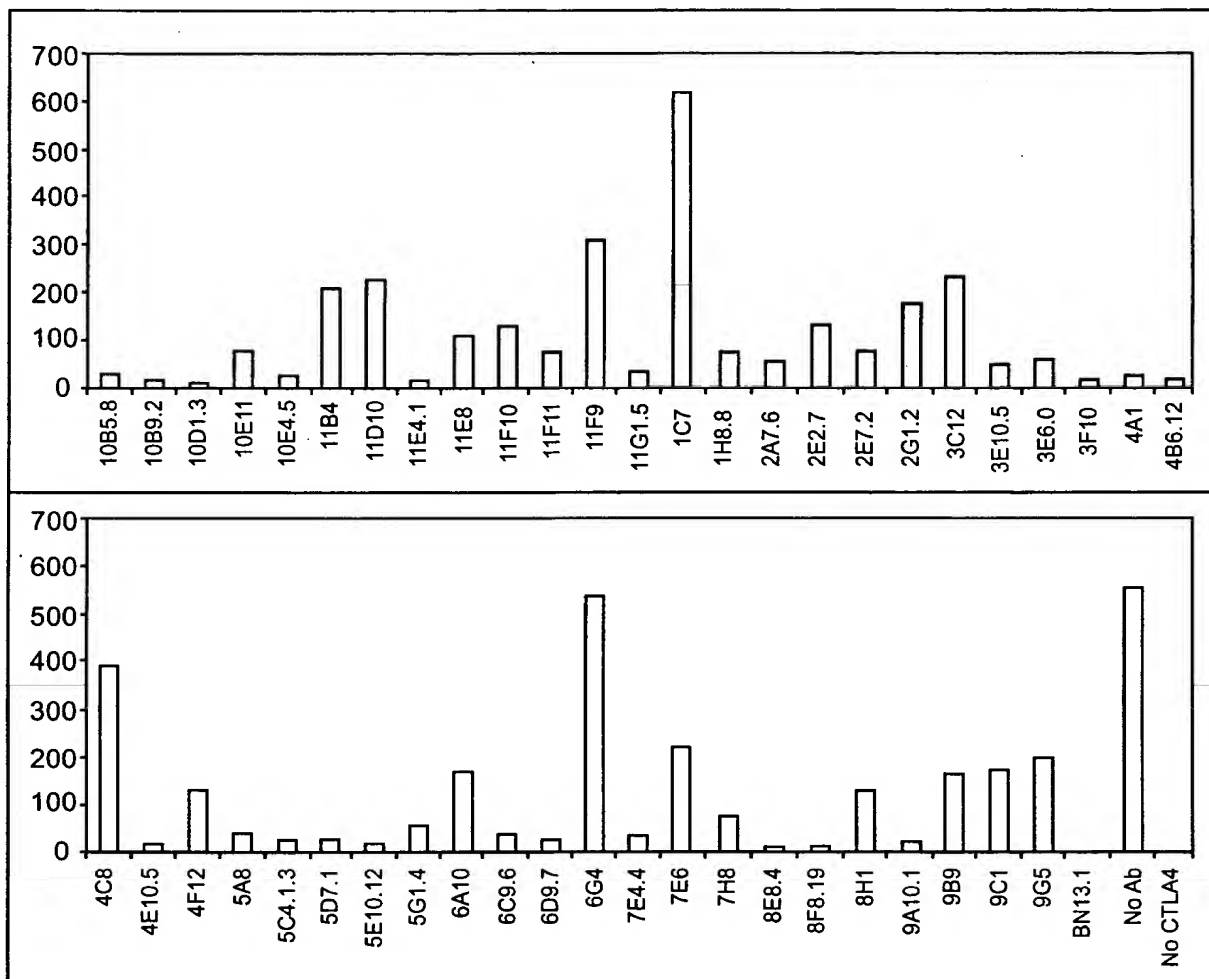


FIG. 2

APPROVED	C.	FIG.
BY	CLASS	SUBCLASS
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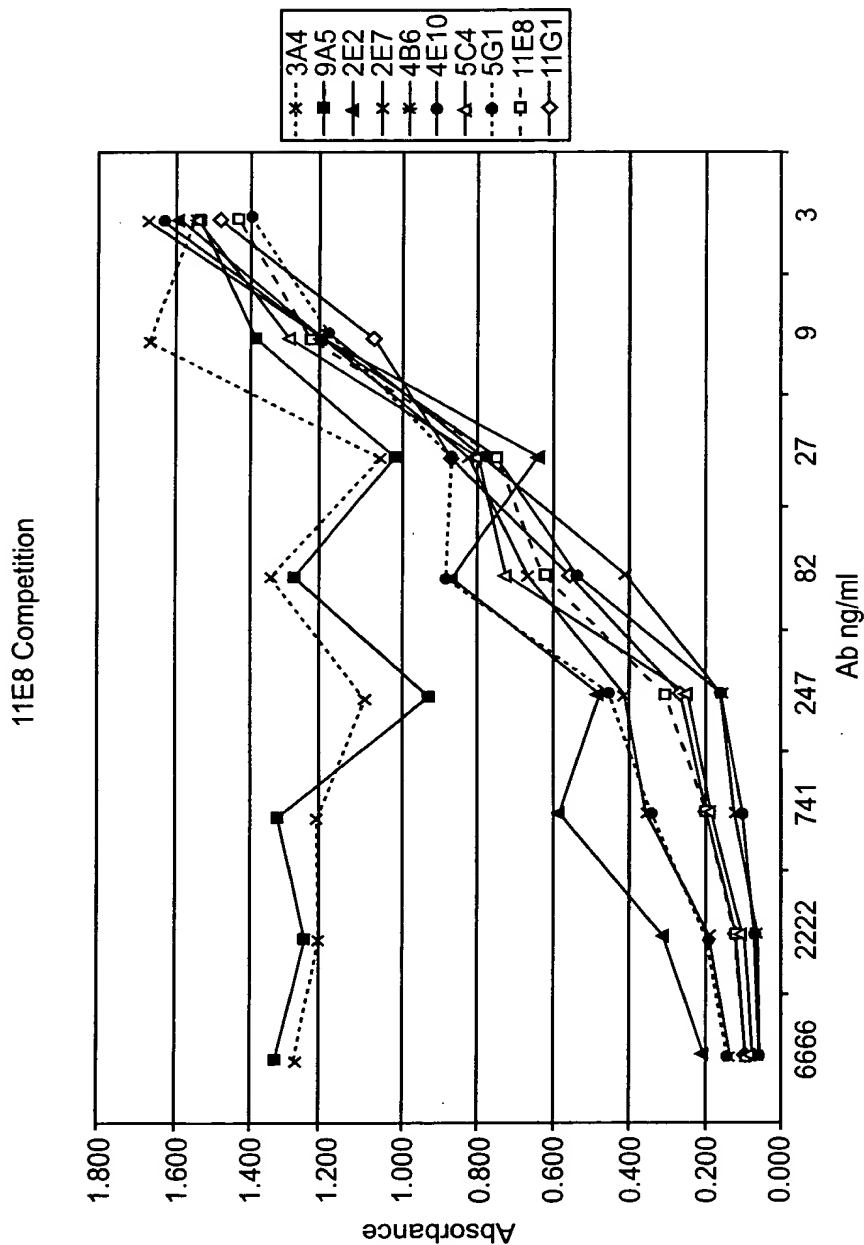
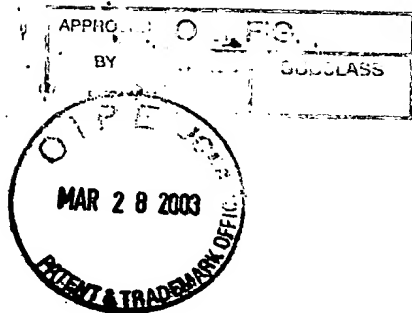


FIG. 3



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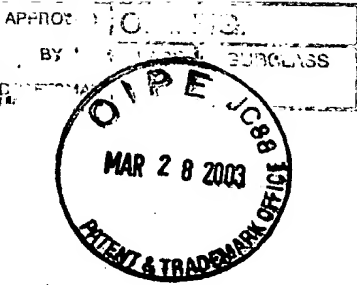
10D1.3 VH (SEQ ID NO:2)

TGGGGGAGGC	GTGGTCCAGC	CTGGGAGGTC	CCTGAGACTC	TCCTGTGCAG	50
CCTCTGGATT	CACCTTCAGT	AGCTATACTA	TGCACTGGGT	CCGCCAGGCT	100
CCAGGCAAGG	GGCTGGAGTG	GGTGACATTT	ATATCATATG	ATGGAAACAA	150
TAAATACTAC	GCAGACTCCG	TGAAGGGCCG	ATTCACCATC	TCCAGAGACA	200
ATTCCAAGAA	CACGCTGTAT	CTGCAAATGA	ACAGCCTGAG	AGCTGAGGAC	250
ACGGCTATAT	ATTACTGTGC	GAGGACCGGC	TGGCTGGGGC	CCTTTGACTA	300
CTGGGGCCAG	GGAACCCTGG	TCACCGTCTC	CTCAGCCTCC	ACCAAGGGC	349

10D1.3 VK (SEQ ID NO:3)

CTCCAGGCAC	CCTGTCTTTG	TCTCCAGGGG	AAAGAGCCAC	CCTCTCCTGC	50
AGGGCCAGTC	AGAGTGTTGG	CAGCAGCTAC	TTAGCCTGGT	ACCAGCAGAA	100
ACCTGGCCAG	GCTCCCAGGC	TCCTCATCTA	TGGTGCATTC	AGCAGGGCCA	150
CTGGCATCCC	AGACAGGTTC	AGTGGCAGTG	GGTCTGGGAC	AGACTTCACT	200
CTCACCATCA	GCAGACTGGA	GCCTGAAGAT	TTTGCAGTGT	ATTACTGTCA	250
GCAGTATGGT	AGCTCACCGT	GGACGTTTCG	CCAAGGGACC	AAGGTGGAAA	300
TCAAACGAAC	TGTGGCTGCA	C			321

FIG. 4



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SEQ ID NOS: 4, 6 & 8 (respectively)

VK A-27
Germline: GAA ATT GTG TTG ACG CAG TCT CCA GGC ACC CTG TCT TTG TCT CCA GGG GAA AGA GCC ACC CTC TCC TGC
10D1: ---
4B6: ---
CDR1: ---
VK A-27: AGG GCC AGT CAG AGT GTT AGC AGC AGC TAC TTA GCC TGG TAC CAG CAG AAA CCT GGC CAG GCT CCC AGG
10D1: ---
4B6: ---

CDR2: ---
VK A-27: CTC CTC ATC TAT GGT GCA TCC AGC AGG GCC ACT GGC ATC CCA GAC AGG TTC AGT GGC AGT GGC TCT GGC
10D1: ---
4B6: ---

VK A-27: ACA GAC TTC ACT CTC ACC ATC AGC AGA CTG GAG CCT GAA GAT TTT GCA GTG TAT TAC TGT
10D1: ---
4B6: ---

CDR3: ---
VK A-27: CAG CAG TAT GGT AGC TCA CC
10D1: ---
4B6: ---

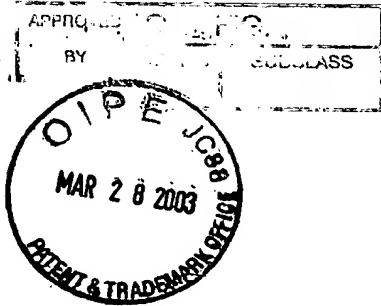
SEQ ID NOS: 10 & 12 (respectively)

VK L-15
Germline: GAC ATC CAG ATG ACC CAG TCT CCA TCC TCA CTG TCT GCA TCT GTA GGA GAC AGA GTC ACC ATC ACT TGT
1E2: ---

CDR1: ---
VK L-15: CGG GCG AGT CAG GGT ATT AGC AGC TGG TTA GCC TGG TAT CAG CAG AAA CCA GAG AAA GCC CCT AAG TCC
1E2: ---

CDR2: ---
VK L-15: CTG ATC TAT GCT GCA TCC AGT TTG CAA AGT GGG GTC CCA TCA AGG TTC AGC GGC AGT GGA TCT GGC ACA
1E2: ---

FIG. 5
1 of 2



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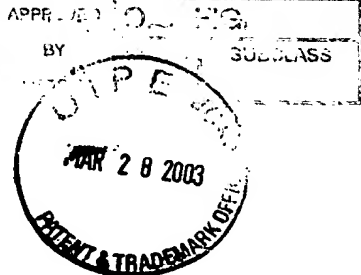
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CDR3 -
VK L-15: GAT TTC ACT CTC ACC ATC AGC AGC CTG CAG CCT GAA GAT TTT GCA ACT TAT TAC TGC CAA CAG TAT AAT
1E2: -----

J_{k1}
VK L-15: AGT TAC CCT CC
1E2: --- --G ACG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C/

FIG. 5
2 of 2



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SEQ ID NOS:14,16&18 (respectively)

VH 3-30.3
Germline: CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG TCC CTG AGA CTC TCC TGT GCA GCC
10D1: ---
4B6: ---

VH 3-30.3: TCT GGA TTC ACC TTC AGT AGC TAT GCT ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG
10D1: ---
4B6: ---

VH 3-30.3: GCA GTT ATA TCA TAT GAT GAT GGA AGC AAT AAA TAC TAC GCA GAC TCC GTG AAG GGC CGA TTC ACC ATC TCC AGA
10D1: A-- T-- --G
4B6: A-- T-- --C

CDR3
D7-27 J_H4b

VH 3-30.3: GAC AAT TCC AAG AAC ACG CTG TAT CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCT GTG TAT TAC TGT
10D1: ---
4B6: ---

VH 3-30.3: GCG AGA
10D1: --- --G
4B6: --- --G

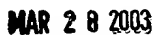
SEQ ID NOS:20&22 (respectively)

VH 3-33
Germline: CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG TCC CTG AGA CTC TCC TGT GCA GCG
1E2: ---

VH 3-33: TCT GGA TTC ACC TTC AGT AGC TAT GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG
1E2: ---

VH 3-33: GCA GTT ATA TGG TAT GAT GGA AGT AAT AAA TAC TAT GCA GAC TCC GTG AAG GGC CGA TTC ACC ATC TCC AGA
1E2: ---

FIG. 6
1 of 2

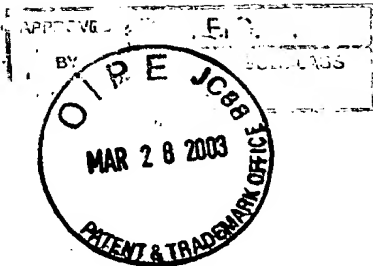


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J_H3b

VH 3-33: GCG AGA GA
1E2: --- --- -CT CCC AAT TAT ATT GGT GCT TTT GAT GTC TGG GGC CAA GGG ACA ATG GTC ACC GTC TCT TCA G/

FIG. 6
2 of 2



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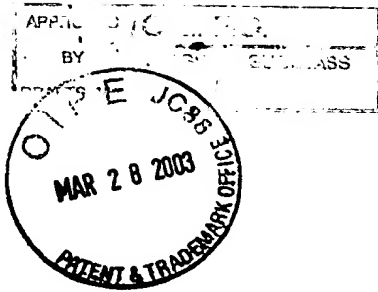
SEQ ID NOS:5,7&9 (respectively)

VK A-27
Germline: EIVLTQSPGTLSPGERATLSC RASQSVSSSYLA WYQQKPGQAPRLLIY GASSRAT
10D1: -----G-----F-----
4B6: -----F-----
CDR1 CDR2
CDR3
VK A-27: GIPDRFSGSGTDFTLTISRLEPEDFAVYYC QQYGSS PWT FGQGTKVEIK
10D1: -----PWT-----
4B6: -----

SEQ ID NOS:11&13 (respectively)

VK L-15
Germline: DIQMTQSPSSLASVGDRTITC RASQISSWLA WYQQKPEKAPKSLIY AASSLQS
1E2: -----
CDR1 CDR2
CDR3
VK L-15: GVPSRFSGSGTDFTLTISLQPEDFATYYC QQYNSY PPT FGQGTKVEIK
1E2: -----PPT-----

FIG. 7



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SEQ ID NOS:15,17&19 (respectively)

VH 3-30.3
Germline: QVQLVESGGGVVQPGRSRLSLCAASGFTFS SYAMH WVRQAPGKGLEWVA VISYDGSNKYYADSVKG
10D1: -----T-----T F-----N-----
4B6: -----T-----T F-----H-----

CDR1 CDR2 CDR3

VH 3-30.3: RFTISRDNKNTLYLQMNSLRAEDTAVYYCAR
10D1: -----I----- TGWLGPFDY WGQGLVTVSS
4B6: -----V-----I-----

SEQ ID NOS:21&23 (respectively)

VH 3-33
Germline: QVQLVESGGGVVQPGRSRLSLCAASGFTFS SYGMH WVRQAPGKGLEWVA VIWYDGSNKYYADSVKG
1E2: -----

CDR1 CDR2 CDR3

VH 3-33: RFTISRDNKNTLYLQMNSLRAEDTAVYYCAR
1E2: -----F----- APNYIGAFDV WGQGTMTVTVSS

FIG. 8



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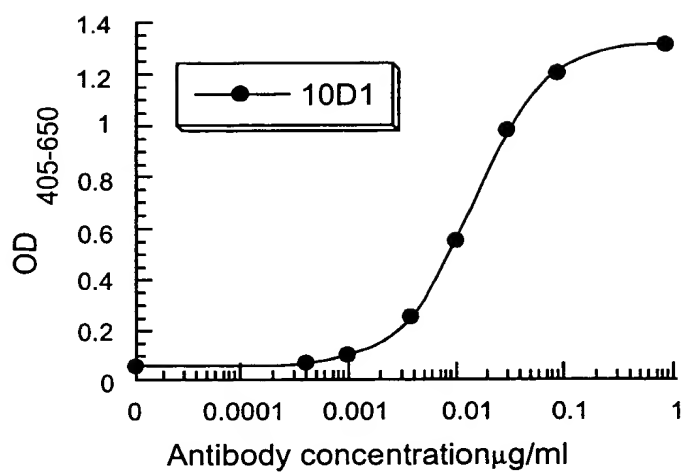
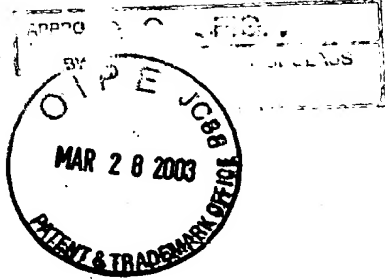


FIG. 9



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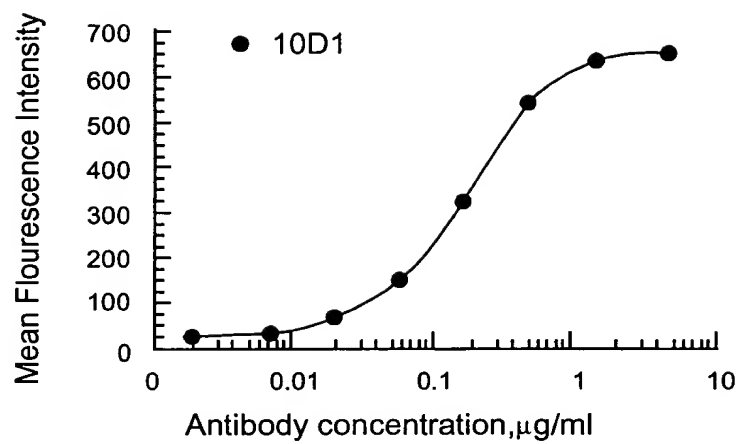
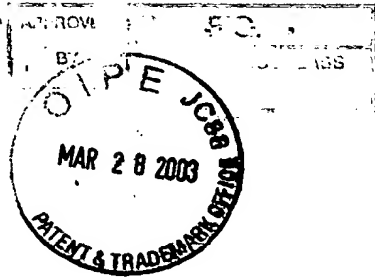


FIG. 10



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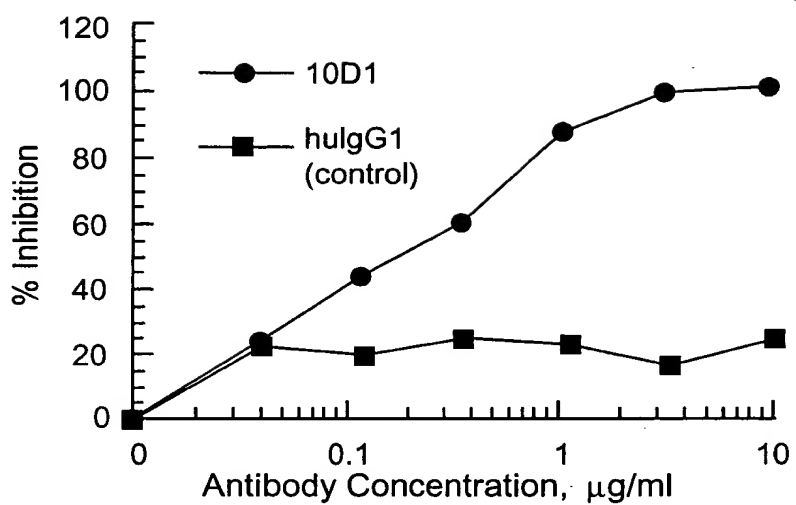
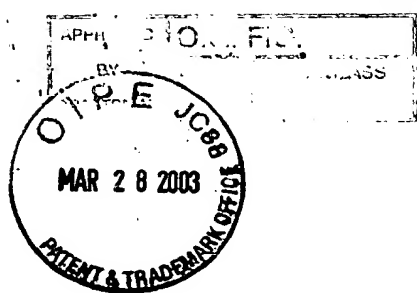


FIG. 11



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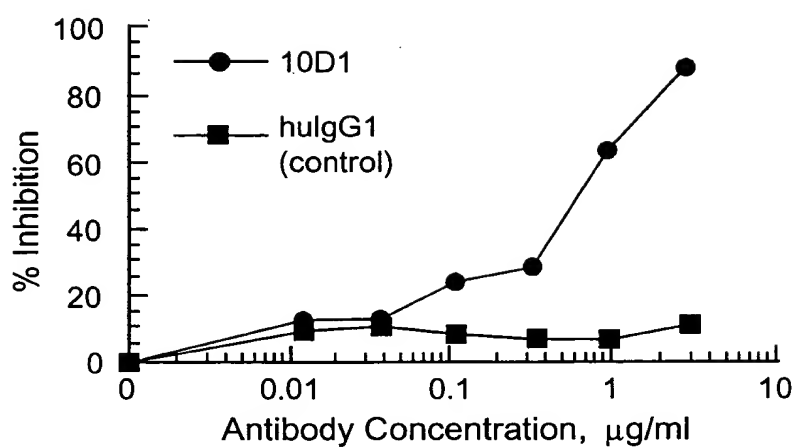


FIG. 12

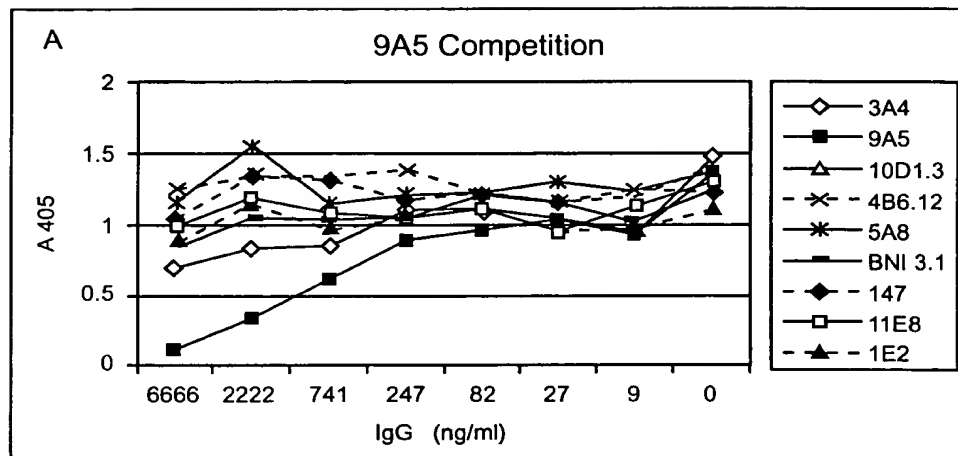


FIG. 13A

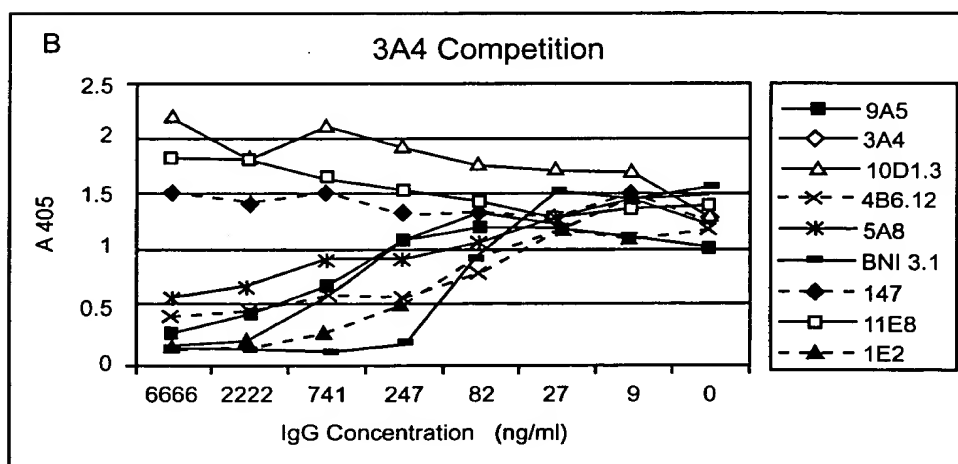


FIG. 13B

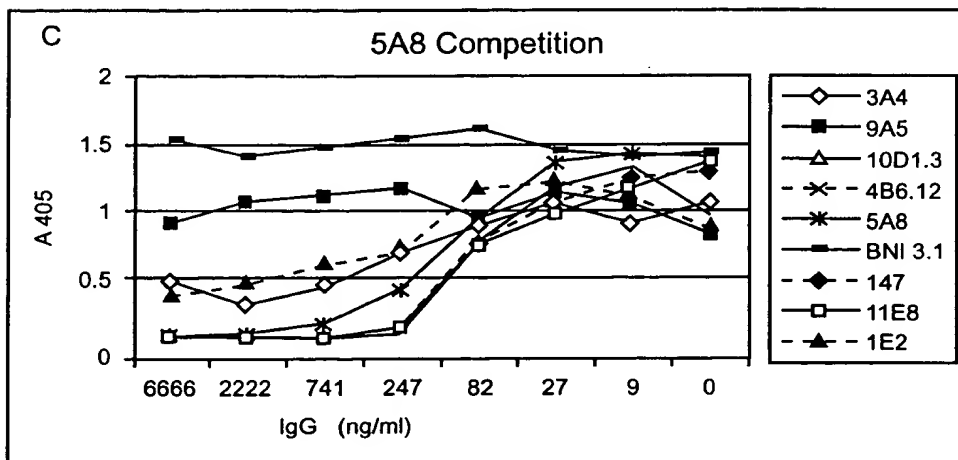


FIG. 13C



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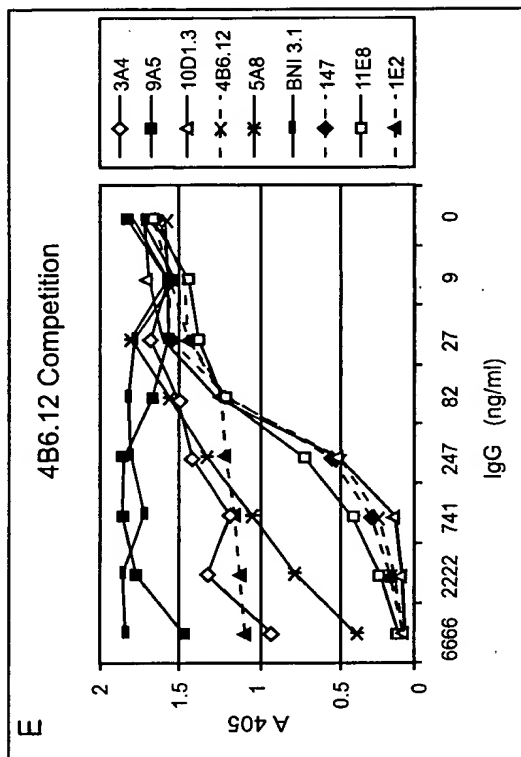


FIG. 13E

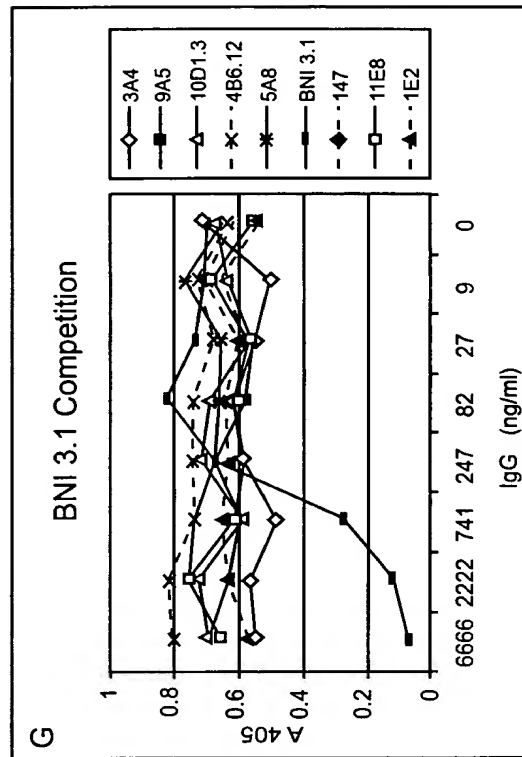


FIG. 13G

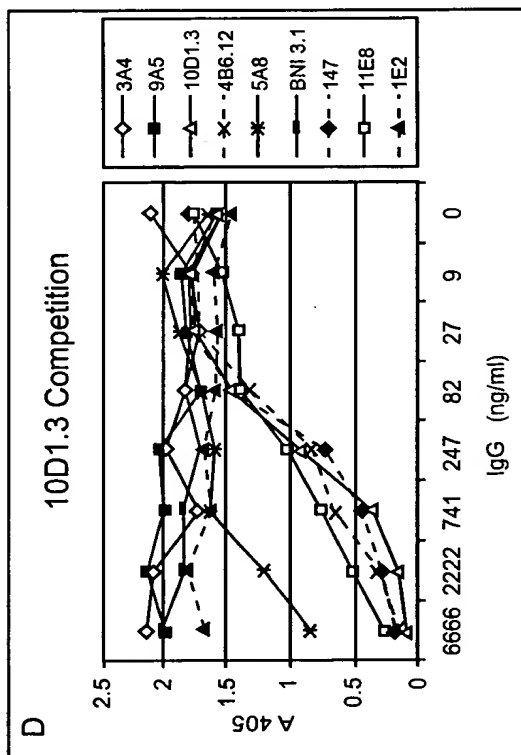


FIG. 13D

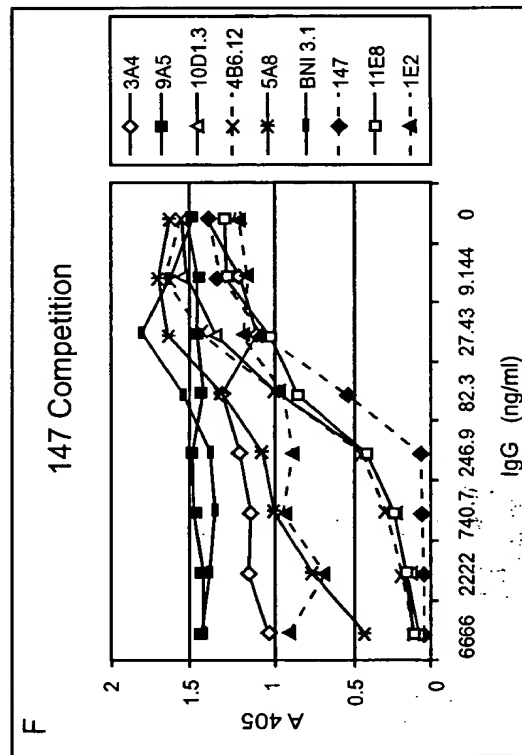


FIG. 13F



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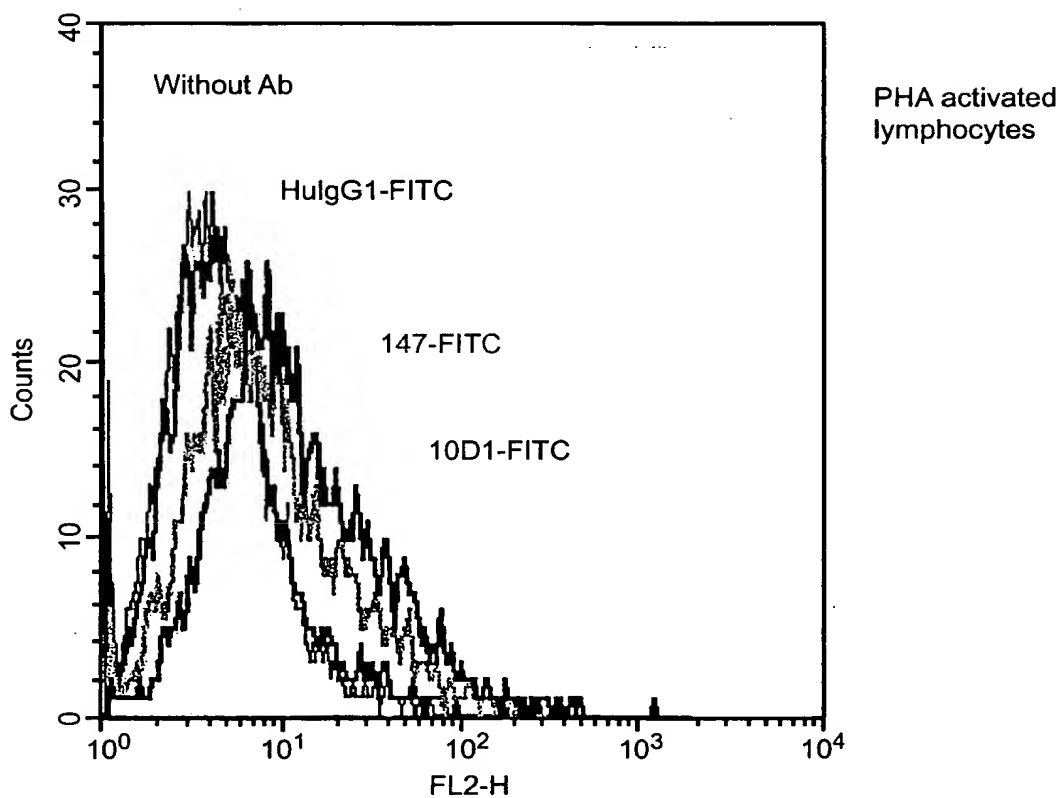
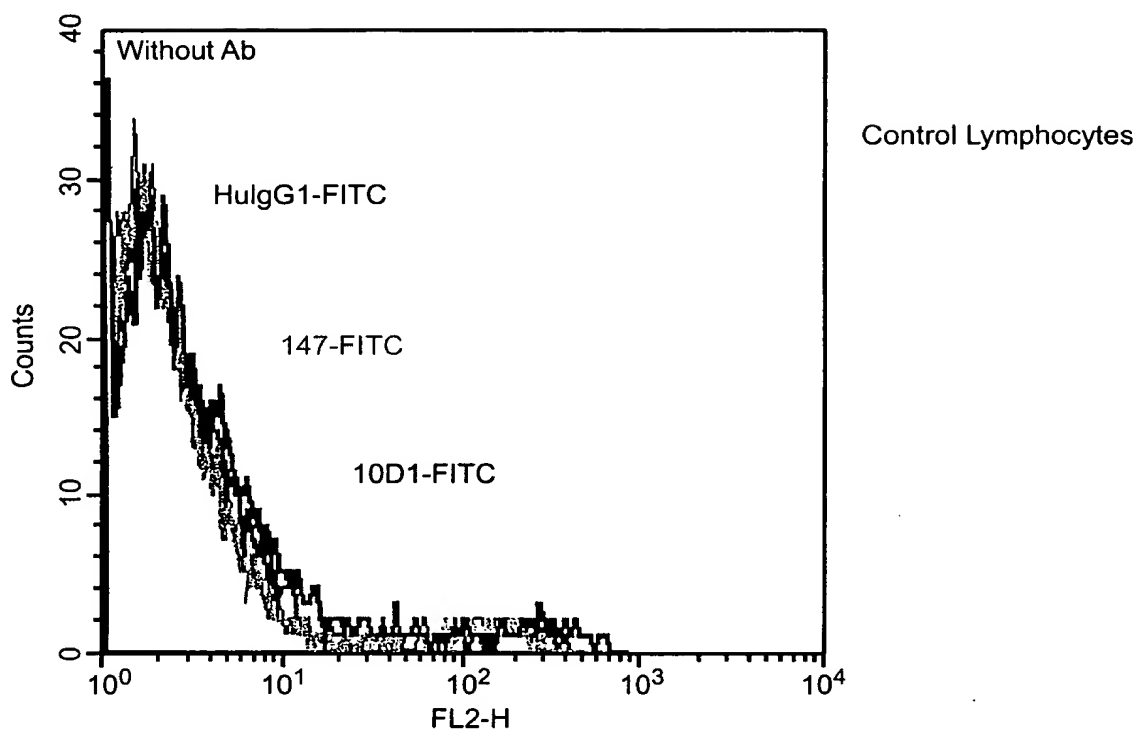


FIG. 14

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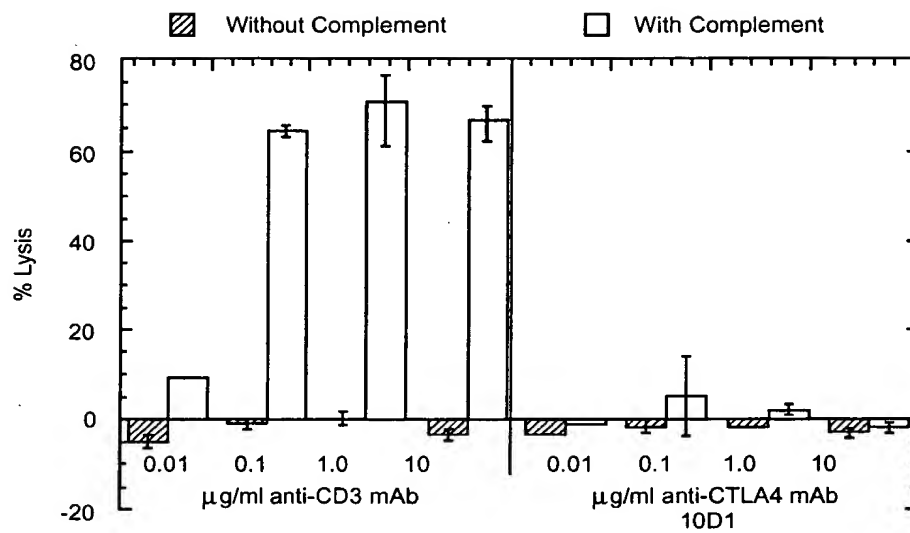


FIG. 15

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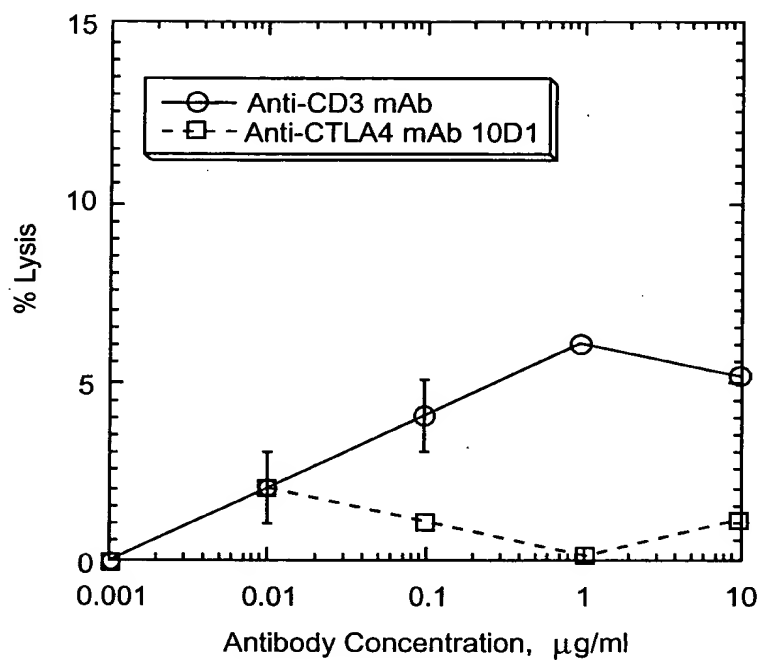


FIG. 16

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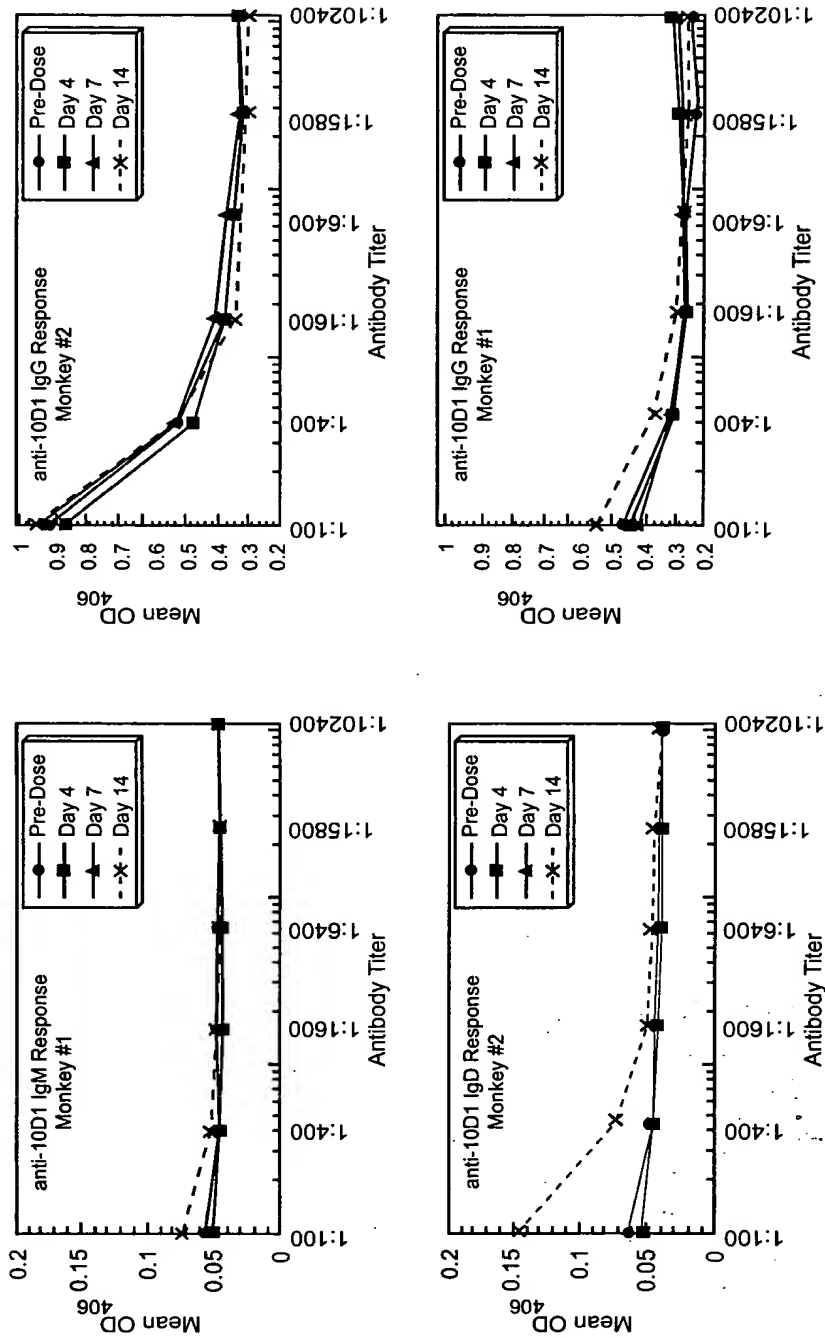
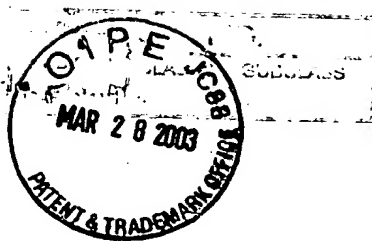


FIG. 17



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Study No. MDXCTLA4-01																					
Selected Lab Values Summary																					
Screen no.	Subject no.	Initials	Amendment #	Day	Date	PSA ng/ml	Platelets x10 ³ /ul	WBC x10 ³ /ul	Neuts %	Lymphs %	Monos %	Eos %	CD4 /ul	CD8 /ul	ESR mm/hr	Hgb g/dl	Hcrit %				
02001	001	JGR		Scr		144.80	263	8.12	73.00	5.90	18.00	1.47	5.60	0.46	1.80	0.15	670	367	71	10.4	30
02001	001	JGR		0		185.20	267	5.74	66.00	3.79	22.00	1.32	6.60	0.38	3.10	0.18	704	376		10.6	32
02001	001	JGR		1			259	6.31	69.00	4.38	20.00	1.29	8.70	0.55	0.90	0.00	A	A		9.5	30
02001	001	JGR		2			240	6.59	70.00	4.66	19.00	1.31	6.70	0.44	1.80	0.12	556	303		9.5	28
02001	001	JGR		3			270	6.53	71.00	4.63	21.00	1.36	5.50	0.36	2.20	0.14	608	254		9.3	28
02001	001	JGR		7		257.40	299	6.70	68.00	4.56	23.00	1.53	6.00	0.40	2.50	0.17	A	A		9.5	28
02001	001	JGR		14		332.30	308	6.87	71.90	7.94	21.20	1.39	5.21	0.36	1.90	0.13	A	A		8.8	25
02001	001	JGR		21			286	9.72	74.00	7.20	19.70	1.91	4.80	0.46	1.00	0.10	A	A		9.1	28
02001	001	JGR		28		351.00	304	5.38	63.00	3.40	26.00	1.44	5.80	0.31	2.90	0.16				8.7	25
01002		JWF		Scr		28.30	271	11.60	75.40	8.75	13.60	1.58	5.70	0.66	4.60	0.53	399	189	41	13.9	37
01003		MZB		Scr		12.70	178	5.49	69.00	3.79	19.60	1.08	6.30	0.35	2.70	0.24	325	168	19	12.7	36
01004		TEQ		Scr		1459.00	264	6.26	75.10	4.70	14.40	0.90	7.70	0.48	2.40	0.15	365	129	61	12.8	36
01005		WMN		Scr		192.40	212	6.85	73.70	5.05	17.40	1.20	6.20	0.43	2.20	0.15	483	217			
01006		MRS		Scr		4503.00	140	7.55	76.70	5.79	15.90	1.20	6.20	0.47	0.80	0.06	319	363	83		
01007		TAB		Scr		1394.00	205	5.78	73.00	4.24	13.00	0.76	6.50	0.37	6.00	0.35	376	127		14.1	43
01008		CHB		Scr		70.70	229	4.67	54.00	2.56	32.00	1.52	8.30	0.39	3.40	0.16	461	499		15.6	45
01009	003	RAB		Scr		238.60	144	3.70	78.00	2.88	14.00	0.55	5.40	0.20	1.20	0.04	211	162	43	9.8	30
01009	003	RAB		0		336.90	123	3.92	68.00	2.67	21.00	0.83	8.70	0.34	1.50	0.06	374	188		10.9	31
01009	003	RAB		1			122	3.35	71.00	2.38	22.00	0.74	4.00	0.14	1.80	0.06	307	192		11.3	32
01009	003	RAB		2			109	4.05	74.00	2.99	19.00	0.77	4.80	0.20	1.20	0.05	328	220		11.3	33
01009	003	RAB		3			114	3.79	70.00	2.67	21.00	0.81	6.20	0.23	1.30	0.05	313	265		10.9	31
01009	003	RAB		7		249.30	69	3.38	75.00	2.54	17.00	0.60	5.60	0.19	0.70	0.02	244	161		10.4	30
01009	003	RAB		14		269.80	101	3.68	69.00	2.54	21.20	0.78	8.50	0.31	1.00	0.04	308	173		8.8	25
01009	003	RAB		21			122	4.82	78.00	3.76	13.20	0.64	7.70	0.37	0.60	0.03	218	195		7.4	20
01012	004	CEH		Scr		112.90	172	5.85	64.00	3.74	28.00	1.69	5.60	0.33	1.00	0.06	746	451	10	13.2	40
01012	004	CEH		1													642	475			
01012	004	CEH		2			150	4.82	67.70	3.26	26.40	1.28	4.60	0.22	1.10	0.05	552	380		12.2	36
01012	004	CEH		3			147	4.36	63.70	2.78	29.30	1.28	5.10	0.22	1.30	0.06	544	441		13.1	37
01012	004	CEH		7		190.00	159	4.95	58.60	2.90	32.70	1.61	5.90	0.29	2.50	0.12	842	506		12.6	35
01012	004	CEH		14		207.60	199	5.64	63.10	3.55	29.30	1.65	5.70	0.32	1.60	0.09				13.5	38
01013		KJF		Scr		49.10	228	8.53	65.00	5.62	26.00	2.23	5.30	0.46	2.30	0.20	1213	398		13.4	37
02014	002	L-S		Scr		12.70	222	5.65	53.00	3.01	34.00	1.92	7.40	0.42	3.90	0.22	721	439		13.6	40
02014	002	L-S		0		27.50	217	5.88	57.00	3.36	32.00	1.88	8.60	0.50	1.50	0.09	676	389		13.5	38
02014	002	L-S		1			226	5.74	55.00	3.19	35.00	2.04	7.00	0.40	1.40	0.08	632	405		13.6	38
02014	002	L-S		2			223	5.59	55.00	3.09	32.00	1.84	9.80	0.55	1.40	0.08	590	339		13.5	39
02014	002	L-S		3			219	4.89	54.00	2.66	34.00	1.68	7.50	0.37	2.70	0.13	529	358		13.2	37
01016	Ineligible	G-F		Scr		4856.00	106	7.31	86.00	6.29	5.00	0.33	6.80	0.49	1.90	0.14	57.6	7		10.3	31
					normal range		150	3.80	40.50	1.96	15.40	0.80	2.60	0.12			404	220			
					low ,																
					high	7.00	10.70	75.00	7.23	48.50	3.00	10.00	0.92	6.80	0.57	1612	1128	30			

TABLE 11

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APR 09 2003

TECH CENTER 1600/2900

Study No. MDXCTLA4-02																				
Selected Lab Values Summary																				
Screen no.	Subject no.	Initials	Amendment #	Day	Date	Platelets x10 ³ /ul	WBC x10 ³ /ul	Neuts %	Neuts x10 ³ /ul	Lymphs %	Lymphs x10 ³ /ul	Monos %	Monos x10 ³ /ul	Eos %	Eos x10 ³ /ul	CD4 /ul	CD8 /ul	ESR mm/hr	Hgb g/dl	Hcrit %
02001	001	SAH	0	Scr		216	6.28	56.60	3.52	35.60	2.23	5.90	0.37	1.80	0.11	1189	631		14.4	39
02001	001	SAH	0	0		230	5.58	59.70	3.33	32.30	1.80	5.70	0.32	1.80	0.10	1039	502		14.9	43
02001	001	SAH	0	1		202	5.12	61.80	3.16	30.20	1.55	5.00	0.26	2.30	0.12	957	407		13.4	37
			normal range		low	150	3.80	40.50	1.96	15.40	0.80	2.60	0.12			404	220			
					high		10.70	75.00	7.23	48.50	3.00	10.10	0.92	6.80	0.57	1612	1129	30		

TABLE 13